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Database :
                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                            US-09-331-631A-8_COPY_33_79
275
1 GDDDPPKRYEDCRRRCEWDT.....QCEESCKSQYGEKDQQQRHR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                March 1, 2001, 16:09:31; Search time 299.73 Seconds (without alignments) 18.379 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                374700 seqs, 117207915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                               sp_mammal:*
sp_mhc:*
sp_organelle:*
                                                                                                                                   sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
  sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                        sp_invertebrate:*
                                                                                                                                                                                                                                                                                                        374700
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Result	Score	%; Query Match	Length	ВС	ID	Description
1	124	45.1	525	10	043358	043358 theobroma C
2	105.5	38.4	593	10	Q9SEW4	
ω	94	34.2	666	10	Q9SPL4	٠.
4	92	33.5	666	10	Q9SPL5	-
5	90	32.7	810	10	Q9ZWI3	
თ	88	32.0	625	10	Q9SPL3	ω
7	82.5	30.0	393	10	Q9ZTPO	
œ	67.5	24.5	541	ഗ	Q9V7P3	Q9v7p3 drosophila
9	65.5	23.8	411	ഗ	P91419	P91419 caenorhabdi
10	65	23.6	554	ഗ	Q9VPS3	Q9vps3 drosophila
11	64	23.3	1298	4	Q9P2D9	
12	63.5	23.1	242	10	081260	081260 tripsacum d
13	63.5	23.1	246	10	081261	081261 tripsacum d
14	62.5	22.7	103	11	Q9J1K0	Q9jikO rattus norv
15	62	22.5	525	υ	Q9VSC2	Q9vsc2 drosophila
16	61.5	22.4	238	10	081255	081255 zea mays su
17	61	22.2	204	ر.	016405	016405 caenorhabdi
18	60.5	22.0	160	10	Q9SQH1	09sqh1 arachis hyp
19	60.5	22.0	238	10	081257	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
9.	9.	9.	9.	9.	9.	59.5	9.	9.	9.	9.	9.	9.	9.	60	60	60	60	60	60	60		•	•	60.5	
•	•		•	•	•	21.6	-			•		•	•			21.8		٠						22.0	
240	240	239	238	238	238	238	238	236	236	230	191	163	122	1927	835	811	774	774	456	241	3469	1819	1327	897	396
10	10	10	10	10	10	10	10	10	10	N	Φ	12				N	N	2	2	Ν	Ŋ	2			
081256	081252	Q9SBF1	09S6Z6	Q9SBE5	Q9SBE8	081258	081249	Q9SBF2	081250	Q9X1D9	Q9N0L8	090098	Q03863	025262	Q9V744	Q926K5	Q9JSK8	Q9K1Z4	Q9Z9G3	Q9K1Y2	Q9U4I2	Q9ZLV0	Q9NFB4	Q17336	Q9NSJ1
zea mays	zea mays	zea		zea luxur	zea	ĸ	zea mays	zea mays	0		=		3 zea mays		drosophila	Q9z6k5 chlamydia p	Q9jsk8 chlamydia p	chlamydia	chlamydia		_	Q9zlv0 helicobacte	Q9nfb4 plasmodium	Q17336 caenorhabdi	Q9nsjl homo sapien

ALIGNMENTS

Qy	Qu Be Ma	SQ	FT	DR E	DR R	DR	DR	DR	1 7	R	RT	RA	RX.	ا ر	R R	R C	2 (38	00	SO	O.N	DE	Dī	DT	ΤŢ	AC.	10.00	RESULT
4 DPPKRYEDCRRRCEWDTRGOKEQQCEESCKSQYGEKDQQQ 44 :: : : :: :: :: :	Query Match 45.1%; Score 124; DB 10; Length 525; Best Local Similarity 46.3%; Pred. No. 5.2e-08; Matches 19; Conservative 12; Mismatches 10; Indels 0; Gaps 0;	CHAIN 25 525 VICILIN. SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;	SIGNAL 1 24 POTENTIAL.	; PD081059; -; 1.	PFAM; PF00546; Seedstore_7s; 1.		P02853;	EMBL; X62626; CAA44494.1;	MOI. BIC	coa and cotton raise questions about vicilin evolution.";	"Comparison of the structure and nucleotide sequences of vicilin genes		MEDLINE=92288309; PubMed=1600151;	TISSUE-LEAVES	SPOTTENCE FROM N A.	(1)	NOBI MANTO 2641.	core eudicots; Rosida	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	Theobroma cacao (Cacao).	CSV.		(TrEMBLrel. 15, Last	(TrEMBLrel. 01,	1996 (TrEMBLrel.	Q43358;	A3358 DEFT TMINAPV. DDM. 525	LT 1

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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                           A family of antimicrobial peptides is produced globulin protein in Macadamia integrifolia."; plant J. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9SPL4; PRELIMINARY; O9SPL4; 11, O1-MAY-2000 (TrEMBLrel. 13, O1-MAY-2000 (TrEMBLrel. 13, O1-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSSEW4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jug r 2,
allergen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Juglans regia (English walnut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fagales; Juglandaceae; Juglans.
NCBI_TaxID=51240;
                                                                                                                                               PFAM; PF00546;
SEQUENCE 666
                                                                                                                                                                                                          EMBL; AF161884; AAD54245.1;
HSSP; P02853; 2PHL.
INTERPRO; IPR001113; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=NUT KERNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMP2
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nes 18; Conserv
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1PR001113; -.
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                                                                                                                                               Seedstore_7s;
AA; 78243 MW;
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Pred. No. 1.3e
13; Mismatches
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RESULT
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Best Local Similarity 55...
Conservative
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Q9ZWI3;
01-MAY-1999
01-MAY-1999
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Q9SPL5;
01-MAY-2000
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SEQUENCE
         PFAM; PF00546; Seedstore_7s; PRODOM; PD081059; -; 1. SEQUENCE 810 AA; 97314 MW
                                                                                                                                           Yamada K., Shimada T., Kondo M., Nishimura "Multiple functional proteins are produced of a single precursor by vacuolar processin J. Biol. Chem. 274:2563-2570(1999).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-KUROKANA AMAKURI NANKIN; TISSUE-COTYLEDON;
                                                                                                                                                                                                                                                                                                                                       Cucurbita maxima (Pumpkin) (Winter squabukaryota; Viridiplantae; Embryophyta; Magnoliophyta; eudicoryledons; core eu Cucurbitales; Cucurbitaceae; Cucurbita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      globulin protein in Macadam
Plant J. 0:0-0(1999).
EMBL; AF161883; AAD54244.1;
HSSP; P02853; 2PHL.
                                                                                              EMBL; AB019195; BAA34056.1; HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marcus J.P., Goulter K.C., Green J.L., Manners J.M.; "A family of antimicrobial peptides is produced by p globulin protein in Macadamia integrifolia kernels."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macadamia integrifolia (Macadamia nut)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMP2
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                                                                                                                                                                                                                                 MEDLINE=99107919; PubMed=9891029;
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPRO01113; -
                                                                              NTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00546; Seedstore_7s;
VCE 666 AA; 78217 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                          IPR001113; -
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A: 97314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
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Last annotation updat
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               A829A3F7542266AB
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annotation updat
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by cleaving Asn-Glr
ng enzyme.";
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Best Local
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Marcus J.P., Goulter K.C., Greer
"A family of antimicrobial pepti
globulin protein in Macadamia ir
Plant J. 0:0-0(1999).
EMBL; AP161885; AAD54246.1; -.
                                                                                                                                                                                                                                                                                                                             01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Trac
Maanollophyta; eudicotyledons; Proteaceae;
                                                                                                                                       STRAIN=LOMELLO;
Chen P.W., Chen L.J.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF049348; AAD02494.1; -.
                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
HYPOTHETICAL 45.3 KDA P
                                                                                                         Hypothetical protein. SEQUENCE 393 AA; 4
                                                                                                                                                                                                                                  Magnoliophyta; I
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                             Q9ZTP0
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01-OCT-2000
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VICILIN PRECURSOR
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GDDDPPKRYEDCRRRCEWDT-RGQKEQQQCEESC--KSQYGEKDQQQRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQQQYEQCQKRCQRRETEPRHMQTCQQRCERRYEKEKRKQQKR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P02853;
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                                Conservative
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13, Last sequence up
15, Last annotation
                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta; Spermatophyta;
                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green J.L., Manners J.M.;
peptides is produced by p
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Last annotation update)
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Pred. No. 0.00
(3; Mismatches
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Pred.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boyle C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brandon R.C., Boyle C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bedshev S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Chambel S.D., Delcher A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Bouston A.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
RA Mountt S.M., Moy M., Murphy B., Murphy D.M., Nelson K.A.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M...
                                                                                                                                                                Query Match
Best Local
                                                                                                                                    Matches
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Q9V7P3;
01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., spier E., Spradling A.C., Stapleton M., Strong R., Sun E., svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X. Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A. Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287.2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese Ralazzolo K., Remington K., Sainders R.D.C., Scheeler F., Shen H.
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Pterygota; Neoptera;
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                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                             FLYBASE;
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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      234
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                                                                       N
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                                                         DDDPPKRYEDCRRRCEWDTR---GQKEQQQCEESCKSQYGEKDQQQRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRRDPKEELRWCKKQCRWEAGQDQRQLRECEEQCLQRQQEDDDDDENTH
                                                                                                                                                                                                                                                                                              AE003807; AAF58004.1; SE; FBgn0034121; CG6262.
NCE 541 AA; 58080 MW;
                                                                                                                                        19;
                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O (TrEMBLrel. 13,
O (TrEMBLrel. 13,
O (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanogaster (Fruit fly).
                                                                                                                                 Conservative
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-DC--ECSMDERQKQQMEQQQKQQDCMRQ--QQQQQQEHQ
                                                                                                                                                                24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endopterygota; Diptera; Brachycera; Muscomorpha; ilidae; Drosophila.
                                                                                                                                                                                                                                                                                                 M.
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Last sequence update)
Last annotation update)
                                                                                                                          Score 67.5; In Pred. No. 0.8; S; Mismatches
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                                                                                                                                                                                                                                                                                              83BEA5FE510F7C8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yao Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang X.,
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PARAMETER OF THE PARAME
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                             Q9VPS3 PRELIMINARY;
Q9VPS3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
STRAIN=BERKELEY;
MEDLINE=20196006;
Adams M.D., Celnii
                                                                                                                                                        Ephydroidea;
                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Diptera
                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                          CG2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U80455; AAB37887.1; -.
SEQUENCE 411 AA; 44675 MW; 599DAC9DCFAB1382 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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STRAIN=BRISTOL Na;
STRAIN=BRISTOL Na;
Wohldmann
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                                                                          SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 EDCRRRCEWDTRGQKE-QQQCEESCKS--QYGEKDQQQR 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDCQAACPQQQQPQQQCQQQCQTTCQSDDQYSQQLIQQQ
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0006; PubMed=10731132; Celniker S.E., Holt R.A.,
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                                                                                                                                                   eoptera; Endopterygota; Diptera;
Drosophilidae; Drosophila.
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Last annotation update)
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Pred. No. 1.1;
11; Mismatches
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Last annotation update)
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Evans C.A.,
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                                                                                                                                                                                                 Hexapoda;
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                                                                                                                                                                       Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
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Gocayne
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                                                                                                                                                                                              Insecta;
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J.D.,
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RA George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Buton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxtendale J., Bayraktargulu L., Becasley E.M.,
RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Belshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botther A., Charler R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botther A., Charler R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Goder C., Gabrielian A.E., Garg N.S., Gelbart H.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lin X., Mattel B., Molintosh T.C., McLeod M.P., Mochrefi A.,
RA Merkhilov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Merkhilov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Palazzolo M., Pettor C., Turner R., Venter E., Wa
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Q9P2D9;
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-OCT-2000 (TrEMBLrel. 15,
Q1-OCT-2000 (TrEMBLrel. 15,
                      TISSUE=BRAIN;
Nagase T., Kikuno R.,
                                                             SEQUENCE FROM N.A
                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                             Homo sapiens (Human)
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Prediction of the coding sequences of unidentified human genes.XVI.
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TE; PS50041; C_TYPE_LECTIN_2; 1.
ER 554 554
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                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 12
 SEQUENCE FROM N. A.
Hilton H., Gaut B.S.;
Hilton H., Gaut B.S.;
"Speciation and domestication in
evidence from the Globulin-1 ge
Genetics 0:0-0(1998).
EMBL; APG64235; AAC31478.1; -.
HSSP; P50477; 1CAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O81260;
01-NOV-1998
01-NOV-1998
01-OCT-2000
                                                                                                                                         GLOBULINI (FRAGMENT).
GLOBULINI (FRAGMENT).
Tripsacum dactyloides (Gama grass).
Tupsacum dactyloides (Bama grass).
Eukaryota; Viridiplantae; Embryophyta; Track
Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                         O81261;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                               081261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Speciation and domestication evidence from the Globulin-1 genetics 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tripsacum dactyloides (Gama grass).
Eukaryota; Viridiplantae; Embryophyta; Traci
Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBL_TaxID=4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF064234; AAC31477.1; -. HSSP; P50477; ICAU. MENDEL; 31902; Trida;1188;31902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00546; Seedstore_7s; 1.
NON_TER 242 242
                                                                                                                                 NCBI_TaxID-4563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [NTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08
                                                                                                                                                                                                                                                                                                                                                                                         12 CRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             large proteins in vitro. Res. 7:65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequences of 150 new large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                           CARRCE--DRPWHQRPRCLEQCREEEREK-QQERSR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDPPKRYEDCRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H., Gaut B.S.;
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12; Conser
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8 (TrEMBLrel.
0 (TrEMBLrel.
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                                                                                                                                                                                                                                                                              PRELIMINARY;
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Last sequence update)
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Last annotation updat
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Pred.
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Pred. No. 1
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                                                       in maize gene.";
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ceae; Tripsacum
                                                                                                                                                             Tracheophyta;
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Q9VSC2
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Best Local
                                                                                                           Pterygota; Neoptera;
Ephydroidea; Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                  STRAIN-BERKELEY
                                                               SEQUENCE FROM N.A.
                                                                                                                                             Drosophila
Eukaryota;
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                                                                                                                                                                                             CG8254 PROTEIN.
                                                                                                                                                                                                                                                                              Q9VSC2
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 Amanatides
                Adams M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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mes 13; Conserv
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les 15; Conserv
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 P.G.,
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103 /
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Celniker S.E., Holt R.A., E
P.G., Scherer S.E., Li P.W.,
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Q9VSC2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
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Q9JIK0;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                 Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
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PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
NON_TER 246 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MENDEL; 31903; Trida;1188;31903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 CRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR 47
                                                                                                                                                                                                                                                                                                                                                        6 PKRYEDCRRRCEWDTR-GQKEQQQCEESCKSQYGEKDQQQRHR
                                                                                                                                                                                                                                                                                                                                         PRQQNSAKARSVWEQRASQLRLQNLRASCEALYSEMDPEERLR
                                                                                                                melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; He
Neoptera; Endopterygota; Diptera;
a; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Last annotation update)
M CHANNEL ALPHAIB (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                               Score 62.5; DB 11;
Pred. No. 0.72;
8; Mismatches 21;
                                                                                                                                                                                                      Last sequence update)
Last annotation updat
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Pred. No. 1.
                                                                                                                                                                                                                                                                  PRT;
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             Evans C.A.
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s C.A., c.
                                                                                                                                             Hexapoda; Insecta;
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                                                                                                                              Brachycera;
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                           Gocayne
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Б.
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Job time: 1577 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA Ballew R.M., Basu A., And H. J., Andrews Franksch C., Bedowin D., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Besch K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dushes R., Dushor R.A., Dong E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeewam C., RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Liu X., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Mang Z.-Y., Wassaman D.A., Wainsers R.D.C., Scheeler F., Shen H., RA Wang Z.-Y., Wassaman D.A., Weinsch M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Shune B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Zheng X.H., Zhou S., Zhon M., Shang G., Zhao Q., Zheng L., Rah Mang Z.-Y., Wassaman D.A., Weinsch S., Zhao Q., Zheng L., Rah J., Rah J., Rah Mang Z.-Y., Shang M., Rah Mang S., Yao Q., Zheng L., Rah
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Best Local S
Matches 16
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PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

SEQUENCE 525 AA; 56769 MW; 2F361B164D982EFE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001356; -. PFAM; PF00046; homeobox; 1.
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                                                                                                                                   467 PKRFEVASGLMLSETQVKIWFQNRRMKW-KRSKKAQQEAKERAKANQQQQQQQQ 519
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16; Conserv
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                                                                                                                                                                                                                                                                    22.5%;
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